

NT1p MGLHAWSEFLKDFLAGAVAAVSKTAVAPIERVKLLLOVQHASKQISAEKQ 50
NT2p MILDAAVSFAKDFLAGGVAAALSKTAVAPIERVKLLLOVQHASKQIIADKQ 50
NT3p MIEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLOVQHASKQIAADKQ 50

NT1p YKGLIDCVVRIPKEQGFLSFWRCNLANVTIRYFPTQALNFAFKDKYKQLEFL 100
NT2p YKGLIDCVVRIPKEQGVLSFWRCNLANVTIRYFPTQALNFAFKDKYKQLEFL 100
NT3p YKGLIDCVVRIPKEQGVLSFWRCNLANVTIRYFPTQALNFAFKDKYKQLEFL 100

NT1p GGVDHFRQFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGRRA 149
NT2p GGVDKFTQFWLYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGRRA 149
NT3p GGVDKHTQFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGRRA 150

NT1p QREFEGLGICLCKKSDGIRGLYQGFNVSVQGIITIRAAVFGVYDTAKG 199
NT2p EREFRGLGICLCKKSDGIRGLYQGFNVSVQGIITIRAAVFGVYDTAKG 199
NT3p EREFRGLGICLCKKSDGIRGLYQGFNVSVQGIITIRAAVFGVYDTAKG 200

NT1p MLPDPKNTHTVSWMTAQTVTAVAGLISYPFDIVRRRMMQSGRKGADIM 249
NT2p MLPDPKNTHTVSWMTAQTVTAVAGLISYPFDIVRRRMMQSGRKGADIM 249
NT3p MLPDPKNTHTVSWMTAQTVTAVAGLISYPFDIVRRRMMQSGRKGADIM 250

ANT1p YTGTVDCWRKIAERDEGCKAFFKCAWSNVLRGMGCAFVLVLYDELKKYV. 298
ANT2p YTGTVDCWRKIAERDEGCKAFFKCAWSNVLRGMGCAFVLVLYDELKKYT. 299
ANT3p YTGTVDCWRKIAERDEGCKAFFKCAWSNVLRGMGCAFVLVLYDELKKVI. 299

Figure 2

104104-0340
T04104-16011860

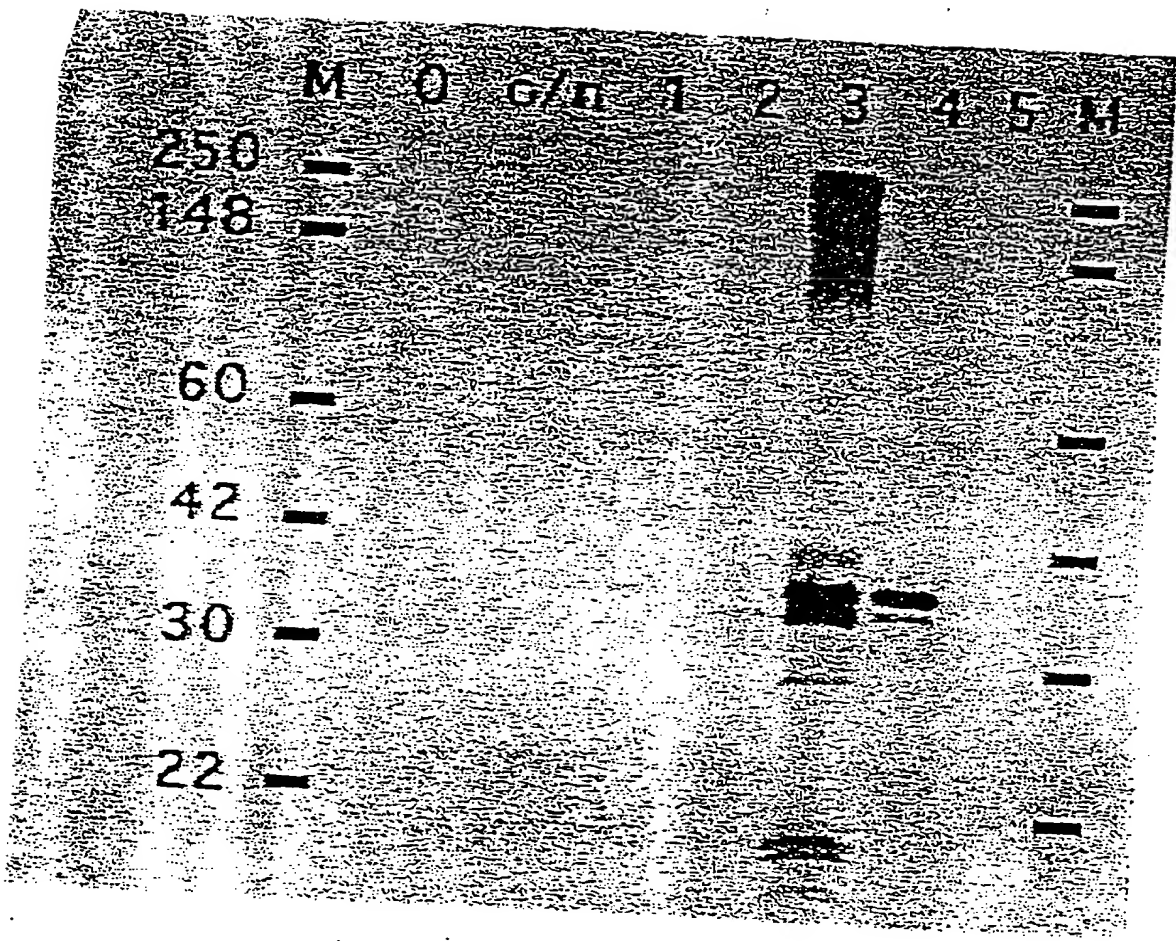


Figure 3

FOOTED-1601860

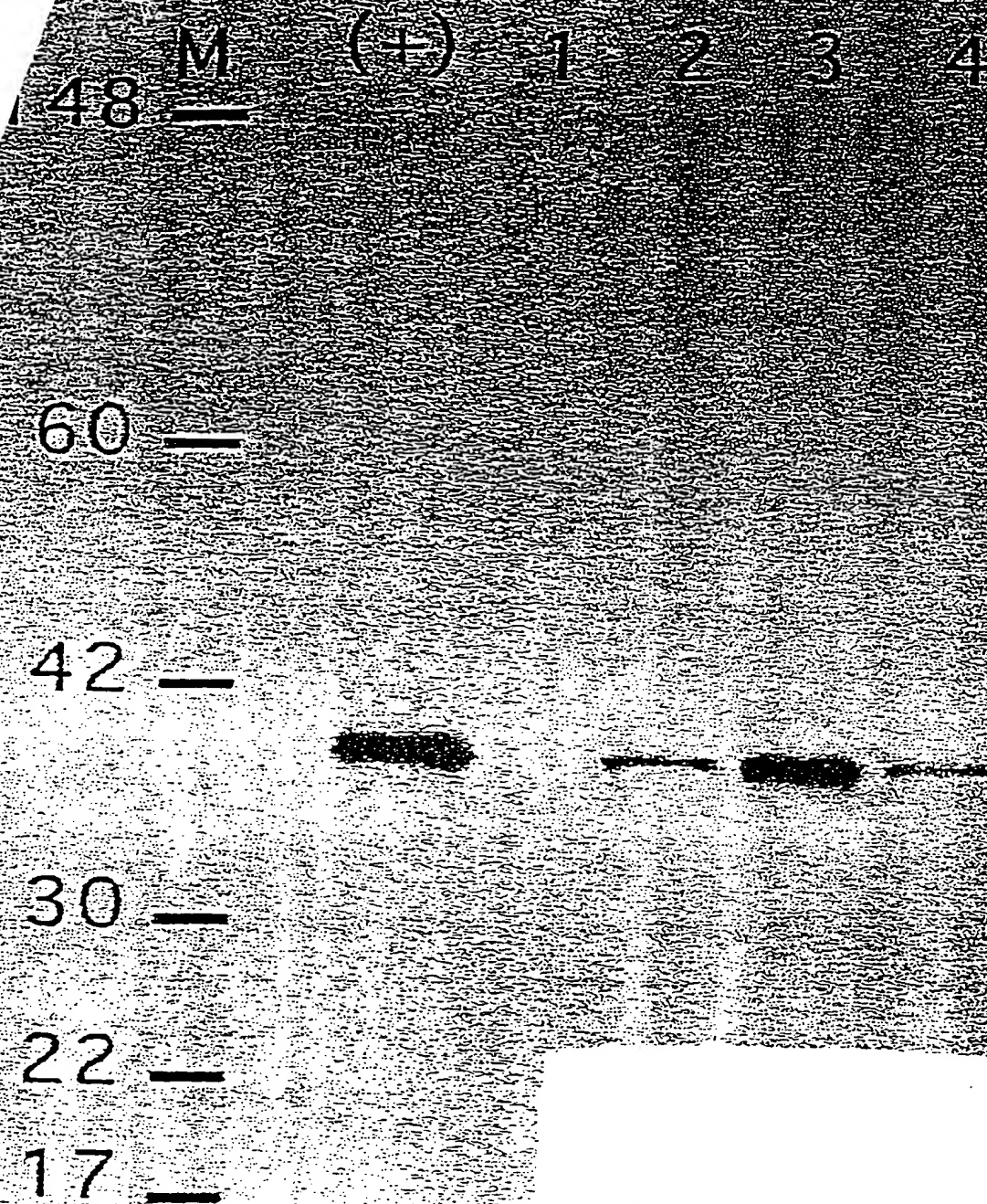


Figure 4

09811094-034401

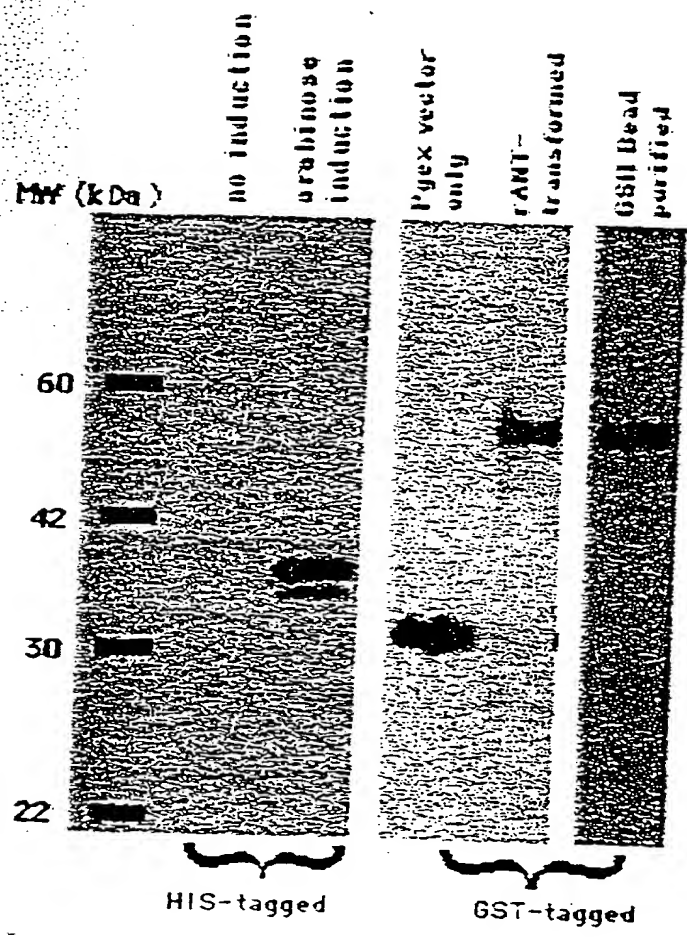


Figure 5

TDH20-160T850

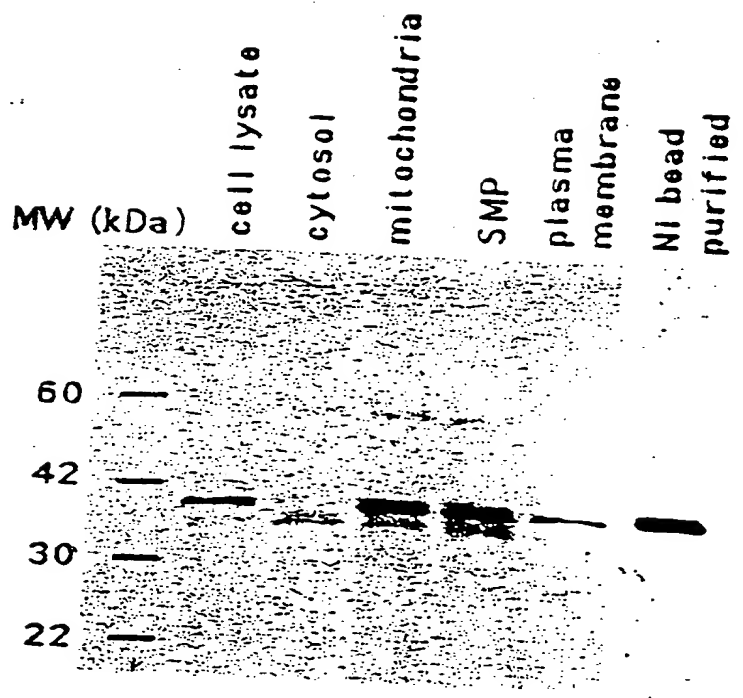


Figure 6

1041120-16011860

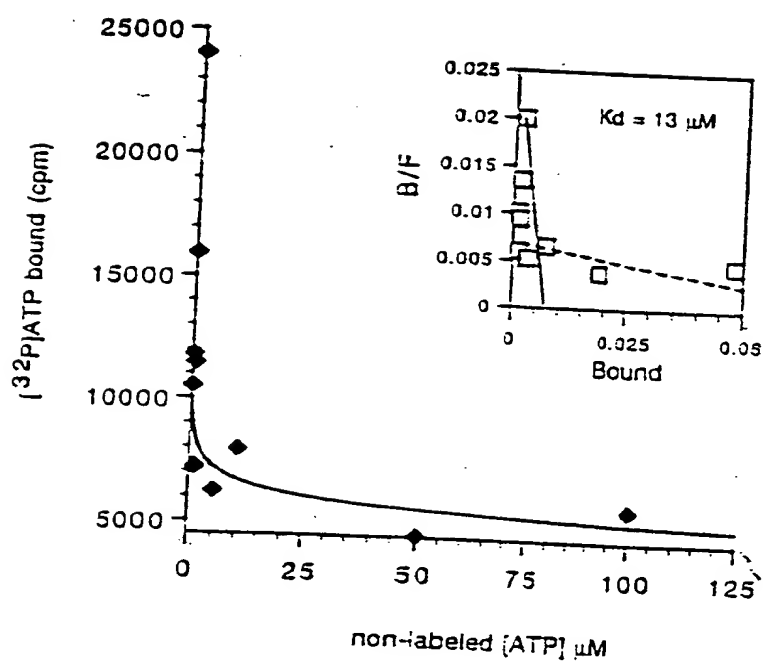


Figure 7

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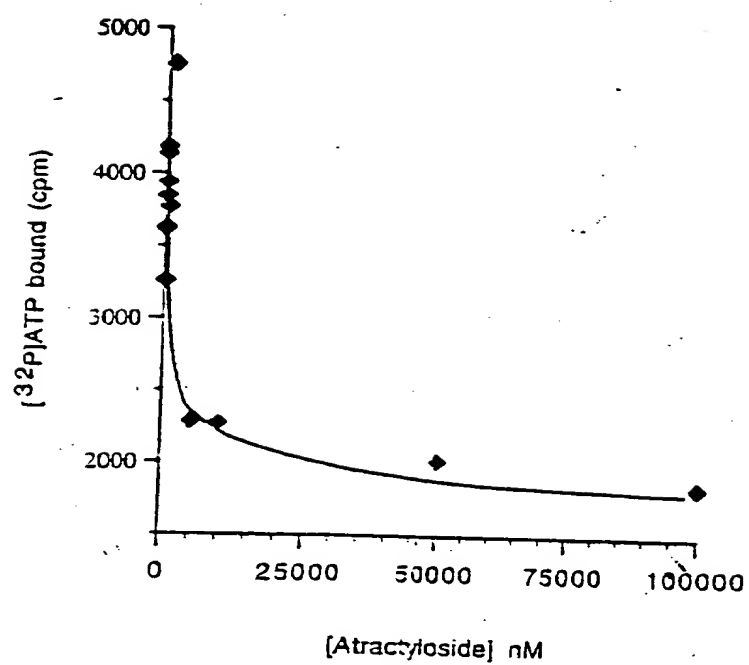


Figure 8

Figure 1 consists of a main binding curve and an inset Scatchard plot. The main plot shows the binding of atracyloside to the ^{125}I -labeled lectin. The y-axis is labeled 'Bound [^{125}I] ATR (cpm)' and ranges from 0 to 250. The x-axis is labeled '[atracyloside] nM' and is on a logarithmic scale from 1 to 10000. The data points, represented by diamonds, show a sigmoidal binding curve that starts at approximately 230 cpm at 1 nM atracyloside, remains relatively flat until about 5 nM, then drops sharply to near zero by 100 nM. An inset Scatchard plot shows the ratio of bound to free ligand (B/F) on the y-axis (0 to 2.5) versus the amount of bound ligand (Bound) on the x-axis (0 to 0.04). The data points in the inset are also diamonds, and a solid line represents a linear fit to the data, with a dashed line indicating the theoretical maximum. The inset is labeled 'Kd = 12 nM'.

Figure 9



Figure 10 -

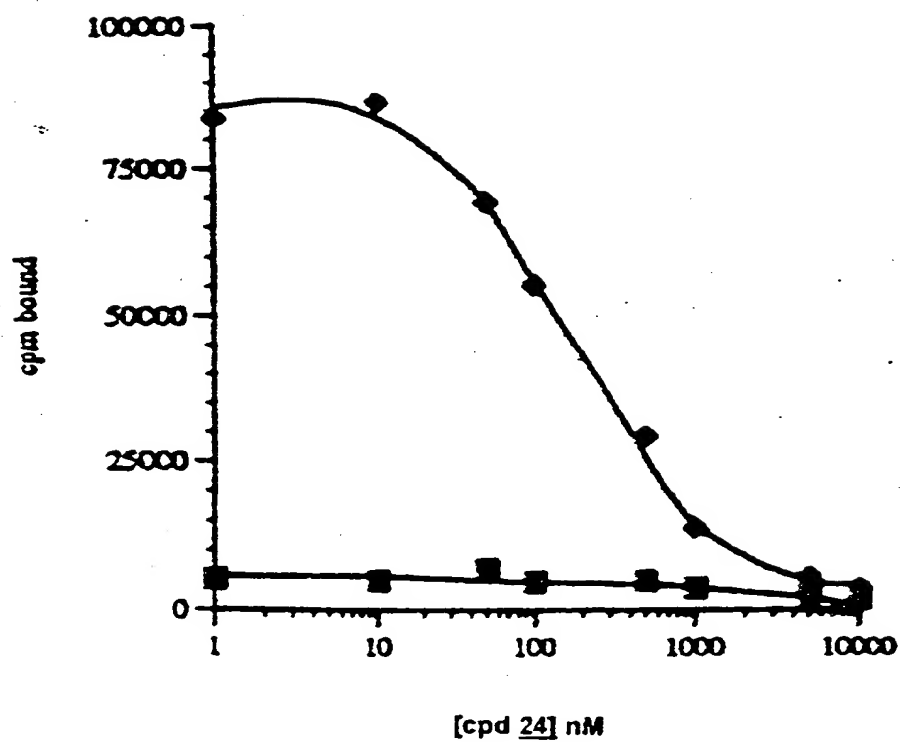


Figure 11

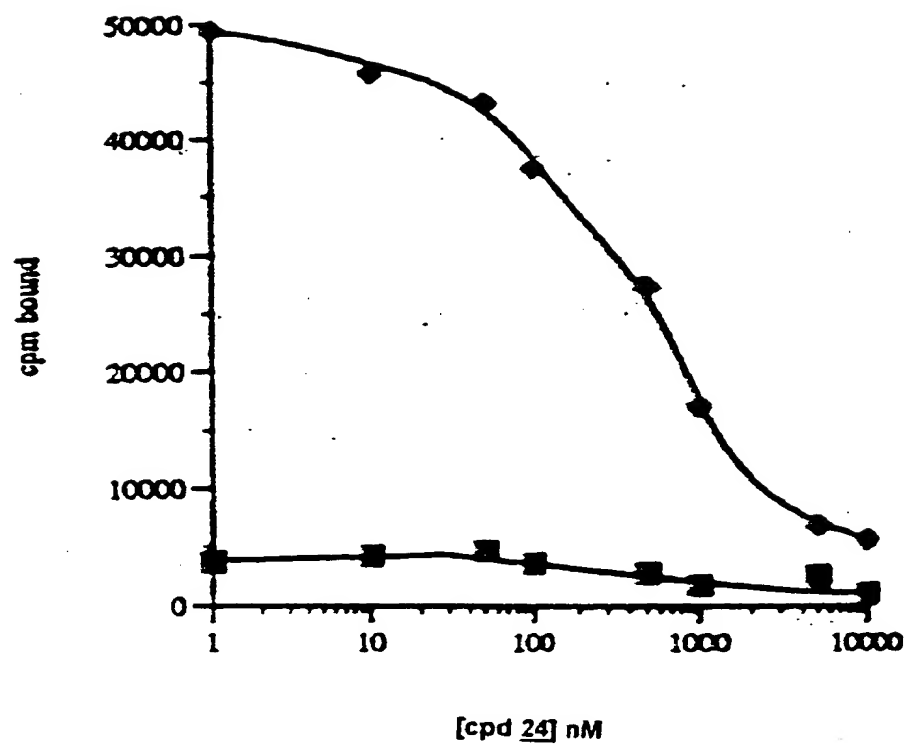


Figure 12

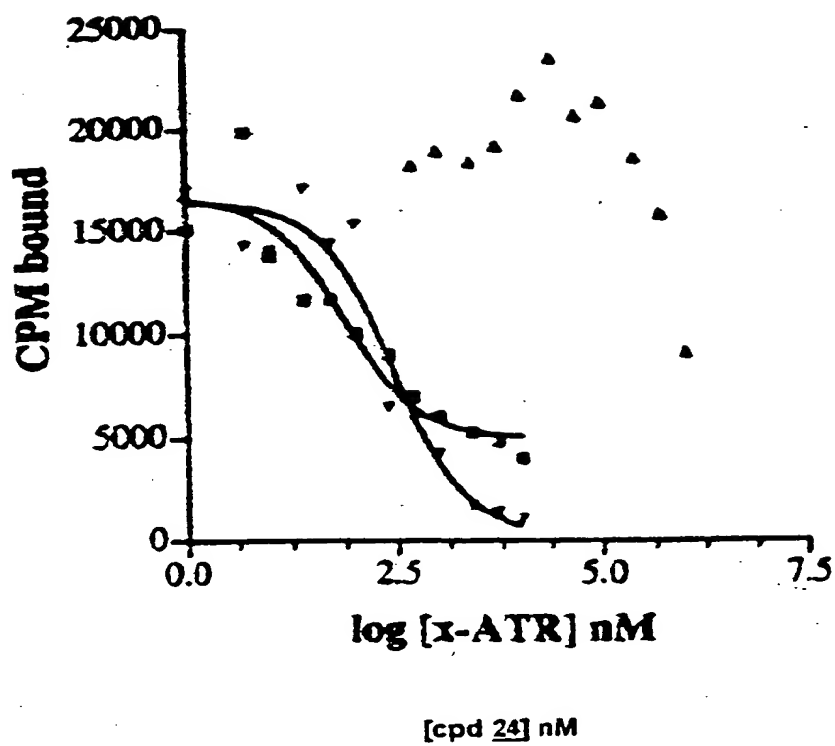


Figure 13

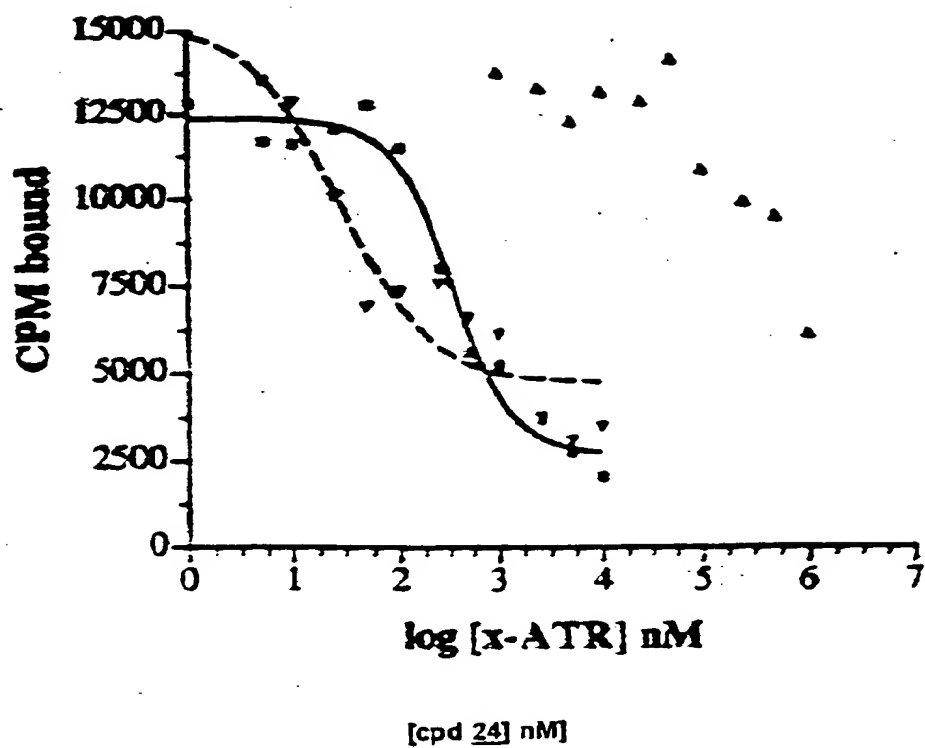


Figure 14

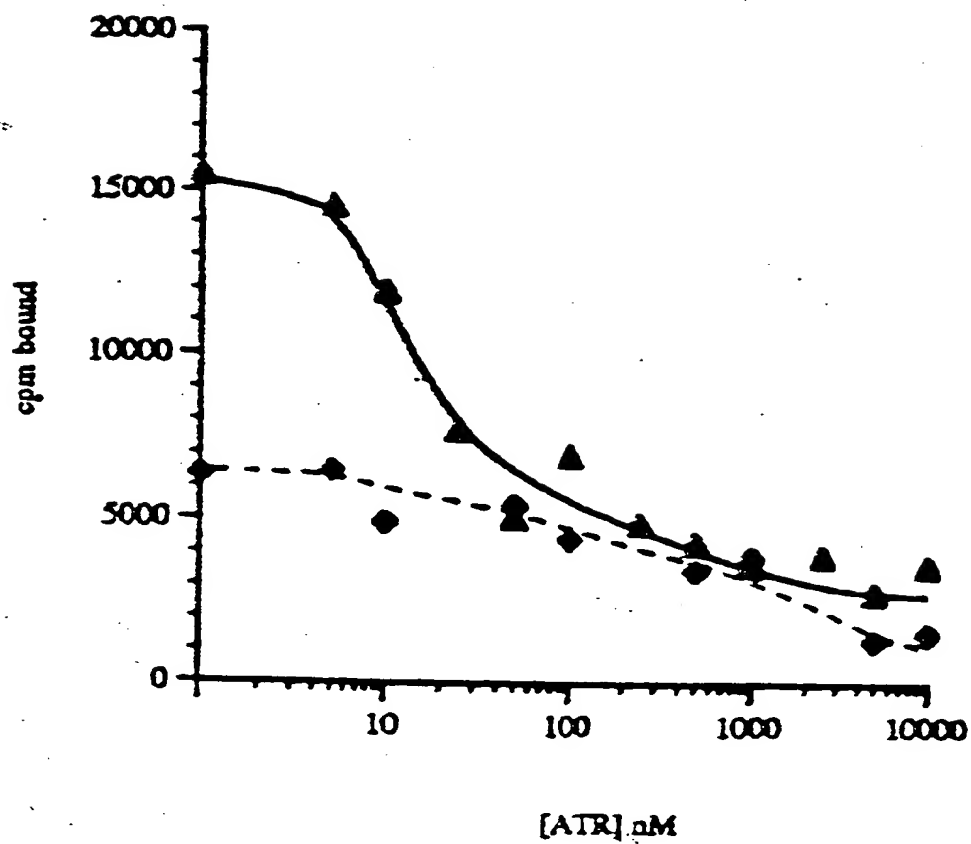


Figure 15

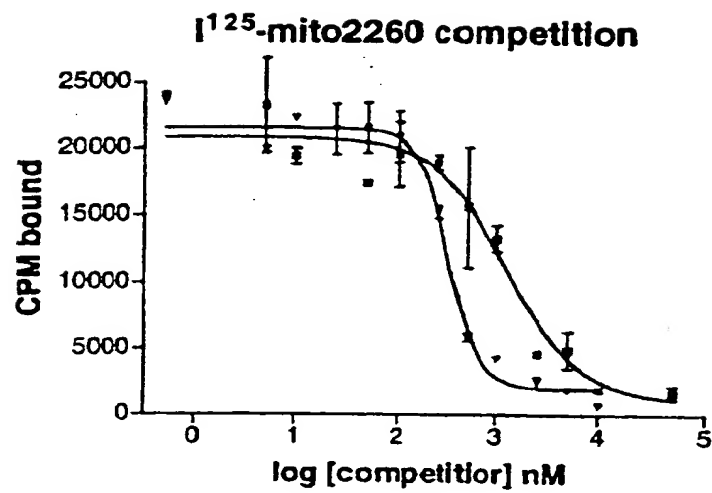


Figure 16

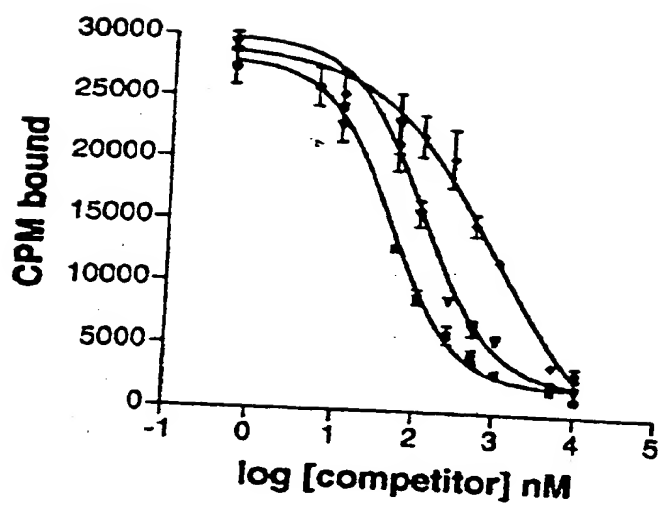


Figure 17

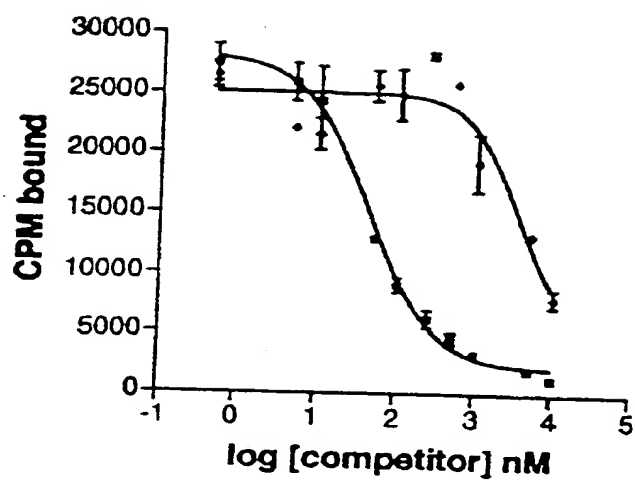


Figure 18

098104 0340
F04T20 460T860

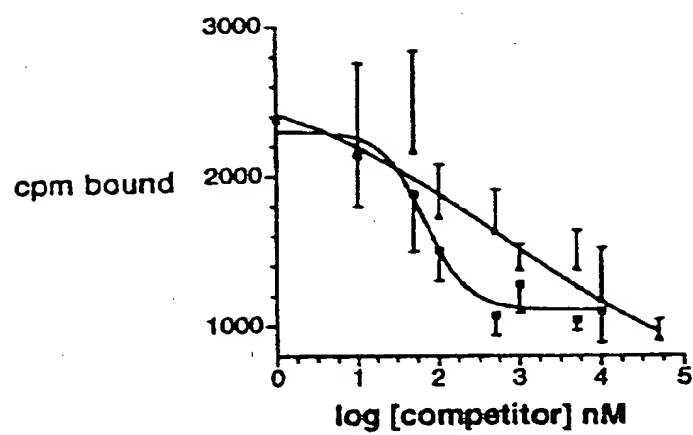


Figure 19